



#5

SEQUENCE LISTING

<110> Allen, Stephen
Kinney, Anthony
Miao, Guo-Hua
Orozco, Emil

<120> PLANT BIOTIN SYNTHASE

<130> BB1429 US NA

<140> US 09/740288

<141> 2000-12-19

<150> US 60/172929

<151> 1999-12-21

<160> 36

<170> Microsoft Office 97

<210> 1
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<212> DNA
<213> Hordeum vulgare

<220>

<221> Unsure

<222> (94)..(94)

<223> n = A, C, G, or T

<220>

<221> Unsure

<222> (460)..(460)

<223> n = A, C, G, or T

<220>

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<222> (462)..(462)

<223> n = A, C, G, or T

<400> 1

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cgcctccgcc	gttagcggccg	cgccttctc	atcggtatcg	gcggccgcgg	cgaggcgcca	180
cgggcgggtgc	gggacggggcc	caggaacgac	tggaccgcgc	ccgagatcca	ggccatctac	240
gactccccgc	tcctcgacct	cctcttccac	ggggctcaag	tccatagaa	tgtccataaaa	300
tttagagaag	tgcacaatcg	cacacttctt	tcaataaaaga	ctgggtgggtg	cagcgaagat	360
tgttcataact	gcccacagtc	ttcaagatac	agtaccggat	tgaaggctga	aaaattaatg	420
aagaaagatg	ccgtcctaga	agcagctaaa	aaggcaaagn	angctgggag	caccgcattt	480
tgattggagc	gatggagaga	gacaattggc	ag			512

<210> 2
<211> 137
<212> PRT
<213> Hordeum vulgare

<220>
<221> UNSURE
<222> (131)..(131)
<223> Xaa = any amino acid

<400> 2
Met Met Leu Leu Leu Ala Arg Ser Leu Arg Ser Arg Val Arg Ser Pro
1 5 10 15
Phe Ala Ser Ala Val Ser Ala Ala Pro Phe Ser Ser Val Ser Ala Ala
20 25 30
Ala Ala Glu Ala Glu Arg Ala Val Arg Asp Gly Pro Arg Asn Asp Trp
35 40 45
Thr Arg Pro Glu Ile Gln Ala Ile Tyr Asp Ser Pro Leu Leu Asp Leu
50 55 60
Leu Phe His Gly Ala Gln Val His Arg Asn Val His Lys Phe Arg Glu
65 70 75 80
Val Gln Gln Cys Thr Leu Leu Ser Ile Lys Thr Gly Gly Cys Ser Glu
85 90 95
Asp Cys Ser Tyr Cys Pro Gln Ser Ser Arg Tyr Ser Thr Gly Leu Lys
100 105 110
Ala Glu Lys Leu Met Lys Lys Asp Ala Val Leu Glu Ala Ala Lys Lys
115 120 125
Ala Lys Xaa Ala Gly Ser Thr Arg Phe
130 135

<210> 3
<211> 496
<212> DNA
<213> Zea mays

<220>
<221> Unsure
<222> (33)..(33)
<223> n = A, C, G, or T

<220>
<221> Unsure
<222> (318)..(318)
<223> n = A, C, G, or T

<220>
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<222> (321)..(321)
<223> n = A, C, G, or T

<220>
<221> Unsure
<222> (365)..(365)
<223> n = A, C, G, or T

<220>
<221> Unsure
<222> (446)..(446)
<223> n = A, C, G, or T

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ccgacgaggc gaggagcgtg caattccgt a gctgcaacga actccctcga ccgtatcgcc 120
cgctgctctt ctatccctt cctgctgctg ctactacctt aagctatcac tatcatggcc 180
ttgatgctgc tagcgcgcaa cctgcgcgtcc cgccctccgccc caccgctcgc cgccgcccgcg 240
gggttctcggt cggccgcggc ggaggcggag agggcgatac gggacgggccc gcggaaacgac 300
tggagccggc ccgagatnca ngccgtctac gactcaccgc tcctcgacct cctctttcac 360
ggggntca gatcaagata caacactgga ttgaagggcc aaaaattgat gaacaaatat 420
gctgtcttgg gagcagcaaa aaaggnaaaa gagtctggga agcaaccgtt tttgcattggg 480
aactgcattt gagaaa 496

<210> 4
<211> 102
<212> PRT
<213> Zea mays

<220>
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<222> (48)..(49)
<223> Xaa = any amino acid

<220>
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<222> (64)..(64)
<223> Xaa = any amino acid

<220>
<221> UNSURE
<222> (91)..(91)
<223> Xaa = any amino acid

<400> 4
Met Ala Leu Met Leu Leu Ala Arg Asn Leu Arg Ser Arg Leu Arg Pro
1 5 10 15
Pro Leu Ala Ala Ala Ala Gly Phe Ser Ser Ala Ala Ala Glu Ala Glu
20 25 30
Arg Ala Ile Arg Asp Gly Pro Arg Asn Asp Trp Ser Arg Pro Glu Xaa
35 40 45
Xaa Ala Val Tyr Asp Ser Pro Leu Leu Asp Leu Leu Phe His Gly Xaa
50 55 60

Gln Ser Ser Arg Tyr Asn Thr Gly Leu Lys Gly Gln Lys Leu Met Asn
 65 70 75 80
 Lys Tyr Ala Val Leu Gly Ala Ala Lys Lys Xaa Lys Glu Ser Gly Lys
 85 90 95
 Gln Pro Phe Leu His Gly
 100

<210> 5
 <211> 497
 <212> DNA
 <213> Zea mays

<220>
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 <222> (192)..(192)
 <223> n = A, C, G, or T

<220>
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 <222> (460)..(460)
 <223> n = A, C, G, or T

<220>
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 <222> (463)..(463)
 <223> n = A, C, G, or T

<220>
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 <222> (469)..(469)
 <223> n = A, C, G, or T

<220>
 <221> Unsure
 <222> (490)..(490)
 <223> n = A, C, G, or T

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 cctcgaccgt atcgccccgt gctcctctat ccctttctgt ctgctgctac taccttaagc 120
 tatcatggcc ttgatgctgc tagcgcgcaa cctgcgctcc cgccctccgccc caccgctcgc 180
 cgccgcccgcg gngttctcggt cggccgcggc ggaggcggag agggcgatac gggacggggcc 240
 gcggAACGAC tggagccggc ccgagattca agccgtctac gactcaccgc tcctcgacct 300
 cctcttcac ggggctcaag tccacagaaa tgtccataaaa ttcaagagaa gtgcagcaat 360
 gcacacttct ttcaatcaag actgggtggga tgcagtgaag attgttctta ctgtcctcaa 420
 gtcatcaaag aataacaacac tgggattgaa gggcccaaann aanttgatna aaaaaagatg 480
 ctgtcttgnn aacaaca 497

<210> 6

<211> 98
 <212> PRT
 <213> Zea mays

<220>
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 <222> (23)..(23)
 <223> Xaa = any amino acid

<220>
 <221> UNSURE
 <222> (72)..(72)
 <223> Xaa = any amino acid

<220>
 <221> UNSURE
 <222> (89)..(89)
 <223> Xaa = any amino acid

<400> 6
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 1 5 10 15
 Pro Leu Ala Ala Ala Ala Xaa Phe Ser Ser Ala Ala Ala Glu Ala Glu
 20 25 30
 Arg Ala Ile Arg Asp Gly Pro Arg Asn Asp Trp Ser Arg Pro Glu Ile
 35 40 45
 Gln Ala Val Tyr Asp Ser Pro Leu Leu Asp Leu Leu Phe His Gly Ala
 50 55 60
 Gln Val His Arg Asn Val His Xaa Ser Arg Glu Val Gln Gln Cys Thr
 65 70 75 80
 Leu Leu Ser Ile Lys Thr Gly Gly Xaa Ser Glu Asp Cys Ser Tyr Cys
 85 90 95
 Pro Gln

<210> 7
 <211> 1152
 <212> DNA
 <213> Zea mays

<400> 7
 gcagccgacg aggcgaggag cgtgcaattc cgtagctgca acgaactccc tcgaccgtat 60
 cgccccgtgc tcctctatcc ct当地ctgct gctgctacta ccttaagcta tc当地tatcat 120
 ggccttgatg ctgctagcgc gcaacctgcg ct当地ccgcctc cgcccacccgc tc当地ccgcgc 180
 cgcggcgttc tcgtcggccg cggcggaggc ggagagggcg atacgggacg ggccgcggaa 240
 cgactggagc cggcccgaga tccaggccgt ctacgactca cc当地ctctcg acctcccttt 300
 tcacggggct caggccaca gaaatgtcca taaattcaga gaagtgcagc aatgcacact 360
 tcttcaatc aagactggtg gatgcagtga agattgttct tactgtcctc agtcatcaag 420
 atacaacact ggattgaagg cccaaaaatt gatgaacaaa tatgctgtct tggaaagcagc 480
 aaaaaaggca aaagagtctg ggagcacccg ttttgcattt ggagctgcattt ggagagaaac 540
 cattggcagg aaatcaaact tcaaccagat tcttgaatat gtcaaggaaa taaggggtat 600
 gggcatggag gtctgttgcacttaggcat gatagagaaa caacaagctg aagaactcaa 660

gaaggctgga	cttacagcat	ataatcataa	cctagataca	tcaagagagt	attatccaa	720
cattattacc	acaagatcat	atgatgatag	actgcagact	cttgagcatg	tccgtgaagc	780
tggaaataagc	atctgctcag	gtggaatcat	tggcttgggt	gaagcagagg	aggaccgggt	840
agggttgg	cataccctag	ctaccttgcc	tacacaccca	gagagcggttc	ctattaatgc	900
attgggttgct	gtaaaaggca	caccttta	ggaccagaag	cctgttagaga	tctggaaat	960
gatccgcatg	atcgccactg	ctcgatcac	gatgccaaag	gcaatggtga	ggcttcagc	1020
aggccgagta	cggctctcg	tgccagaaca	agcgctgtgc	ttctcgctg	gggccaactc	1080
catccttggc	ggcgagaaac	ttctcacaac	cgcaaacaac	gacttgatg	cggaccaagc	1140
gatgttcaag	at					1152

<210> 8
<211> 344
<212> PRT
<213> Zea mays

<400>	8					
Met Ala Leu Met	Leu Leu Ala Arg Asn	Leu Arg Ser Arg	Leu Arg Pro			
1	5	10	15			
Pro Leu Ala Ala	Ala Ala Ala Phe Ser	Ser Ala Ala Ala	Glu Ala Glu			
20	25	30				
Arg Ala Ile Arg Asp Gly	Pro Arg Asn Asp	Trp Ser Arg	Pro Glu Ile			
35	40	45				
Gln Ala Val Tyr Asp Ser	Pro Leu Leu Asp	Leu Phe His	Gly Ala			
50	55	60				
Gln Val His Arg Asn	Val His Lys Phe	Arg Glu Val Gln Gln	Cys Thr			
65	70	75	80			
Leu Leu Ser Ile Lys	Thr Gly Gly Cys	Ser Glu Asp Cys	Ser Tyr Cys			
85	90	95				
Pro Gln Ser Ser Arg	Tyr Asn Thr Gly	Leu Lys Ala Gln Lys	Leu Met			
100	105	110				
Asn Lys Tyr Ala Val	Leu Glu Ala Ala Lys	Lys Ala Lys Glu	Ser Gly			
115	120	125				
Ser Thr Arg Phe Cys	Met Gly Ala Ala Trp	Arg Glu Thr Ile	Gly Arg			
130	135	140				
Lys Ser Asn Phe Asn	Gln Ile Leu Glu	Tyr Val Lys Glu Ile	Arg Gly			
145	150	155	160			
Met Gly Met Glu Val	Cys Cys Thr Leu	Gly Met Ile Glu Lys	Gln Gln			
165	170	175				
Ala Glu Glu Leu Lys	Ala Gly Leu Thr	Ala Tyr Asn His	Asn Leu			
180	185	190				
Asp Thr Ser Arg Glu	Tyr Tyr Pro Asn	Ile Ile Thr Thr	Arg Ser Tyr			
195	200	205				
Asp Asp Arg Leu Gln	Thr Leu Glu His	Val Arg Glu Ala	Gly Ile Ser			
210	215	220				
Ile Cys Ser Gly	Gly Ile Ile Gly	Leu Gly Glu Ala	Glu Glu Asp Arg			
225	230	235	240			
Val Gly Leu Leu His	Thr Leu Ala Thr	Leu Pro Thr His	Pro Glu Ser			
245	250	255				
Val Pro Ile Asn	Ala Leu Val Ala Val	Lys Gly Thr Pro	Leu Glu Asp			
260	265	270				
Gln Lys Pro Val Glu	Ile Trp Glu Met	Ile Arg Met Ile	Ala Thr Ala			
275	280	285				
Arg Ile Thr Met Pro	Lys Ala Met Val	Arg Leu Ser	Ala Gly Arg Val			
290	295	300				
Arg Phe Ser Met Pro	Glu Gln Ala Leu	Cys Phe Leu	Ala Gly Ala Asn			

305	310	315	320
Ser Ile Leu Ala Gly Glu Lys Leu Leu Thr Thr Ala Asn Asn Asp Phe			
325	330	335	
Asp Ala Asp Gln Ala Met Phe Lys			
340			

<210> 9
<211> 562
<212> DNA
<213> Argemone mexicana

<220>
<221> Unsure
<222> (553)..(553)
<223> n = A, C, G, or T

<400> 9			
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gagagctcgt cttcgacctt tgattttcat ttctacattt tcttctctct catcatcttc	180		
ttcttcttca gctgctgctg ttcaaggcaga aagaacgatt aaagaaggc caagaaaacga	240		
ttggagcaga gatgaaaatta aatcggttta tgattctcca gttctcgatc ttctcttcca	300		
tgcagctcaa gtccatagac atgctcacaa cttcagggaa gtgcagcaat gtactcttct	360		
ctctgttaag acaggtgggt gcagtgaaga ttgttcatat tgtccacaat cttccaggta	420		
tgacactgga gtgaaagccc aaaagctgat gaacaaggga cgccaggctg caaggaagca	480		
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tacaatgggg aangaagaac aa	562		

<210> 10
<211> 119
<212> PRT
<213> Argemone mexicana

<400> 10			
Met Leu Lys Val Gln Ser Leu Arg Ala Arg Leu Arg Pro Leu Ile Phe			
1 5 10 15			
Ile Ser Thr Phe Ser Ser Leu Ser Ser Ser Ser Ser Ala Ala			
20 25 30			
Ala Val Gln Ala Glu Arg Thr Ile Lys Glu Gly Pro Arg Asn Asp Trp			
35 40 45			
Ser Arg Asp Glu Ile Lys Ser Val Tyr Asp Ser Pro Val Leu Asp Leu			
50 55 60			
Leu Phe His Ala Ala Gln Val His Arg His Ala His Asn Phe Arg Glu			
65 70 75 80			
Val Gln Gln Cys Thr Leu Leu Ser Val Lys Thr Gly Gly Cys Ser Glu			
85 90 95			
Asp Cys Ser Tyr Cys Pro Gln Ser Ser Arg Tyr Asp Thr Gly Val Lys			
100 105 110			
Ala Gln Lys Leu Met Asn Lys			
115			

<210> 11

<211> 1340
 <212> DNA
 <213> Glycine max

<400> 11

ctagtactgc	tccctctgcg	acttcgttgc	gtagaggat	tttggccgcc	aaataaacag	60
tctcaccata	aactccaaag	tcccaacgct	aaacgaaacc	aaacccaaa	cacaatacc	120
gttgttgct	gttgtctcg	tcgtgttat	attcgagat	ctctcaacta	ttctctgttg	180
tttctctgcc	caacttcgaa	ttcgaaagca	aaaacatgtt	tttggcgaga	cccatttcc	240
gagcacccctc	ccttggcg	ttgactctt	cctacgcgta	ttcctctgcc	tcagcagctg	300
caattcaagc	tgagagagcc	atcaaagaag	gaccaggaaa	cgattggagc	cgagaccaag	360
tcaaatccat	ctacgactct	cccatttcg	atcttctctt	ccatggggct	caagttcaca	420
gacatgctca	taacctcagg	gaagttcaac	agtgtactct	tctgtctatc	aaaacaggag	480
ggtgcagtga	agattgtcc	tattgtcctc	aatcctctaa	gtatgataca	ggagtcaaaa	540
gccaaggct	tatgaacaag	gaagctgttc	tccaggctgc	aaagaaggca	aaagaggctg	600
ggagcactcg	ctttgtatg	gggtctgcgt	ggagggatac	actaggaaga	aagaccaact	660
tcaaccagat	ccttgaatat	gtgaaagaca	taagggacat	gggaatggag	gtttgttgc	720
cccttggcat	gctggagaaa	cagcaggctg	ttgaactcaa	gaaggcaggt	ctcaactgctt	780
ataatcacaa	tcttgacact	tcaaggaggat	attatccaaa	cataatcaca	acaaggactt	840
atgatgagcg	tcttcaaacc	tttgagtttgc	ttcgggatgc	aggatcaat	gtttgttctg	900
gaggaattat	agggcttgg	gaagcagagg	aggatcggt	aggttgtta	catacattgt	960
caacacttcc	caccatcca	gagagtgttc	ctattaatgc	acttggct	gtaaaggaa	1020
ccccttta	ggatcagaag	cctgttggaaa	tatggagat	gattcgatg	atagcaactg	1080
cacgtatcg	aatgcaaaaa	gcaatggtca	ggttatcagc	tggcagagtt	cgattctcca	1140
tgcctgagca	ggcattgtgc	tttcttgcgt	gtgcaaattc	tatattcact	ggtgaaaagc	1200
ttctcaactac	tcctaacaat	gatttgatg	ctgatcaact	catgtttaaa	gttcttggac	1260
ttctcccaa	agctccaagc	ttacatgaag	gtgaaactag	tgtgacagaa	gattataagg	1320
aagcagcttc	ttcttagttga					1340

<210> 12
 <211> 374
 <212> PRT
 <213> Glycine max

<400> 12

Met	Phe	Leu	Ala	Arg	Pro	Ile	Phe	Arg	Ala	Pro	Ser	Leu	Trp	Ala	Leu
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His	Ser	Ser	Tyr	Ala	Tyr	Ser	Ser	Ala	Ser	Ala	Ala	Ala	Ile	Gln	Ala
							20				25		30		
Glu	Arg	Ala	Ile	Lys	Glu	Gly	Pro	Arg	Asn	Asp	Trp	Ser	Arg	Asp	Gln
							35			40			45		
Val	Lys	Ser	Ile	Tyr	Asp	Ser	Pro	Ile	Leu	Asp	Leu	Leu	Phe	His	Gly
							50			55			60		
Ala	Gln	Val	His	Arg	His	Ala	His	Asn	Phe	Arg	Glu	Val	Gln	Gln	Cys
									70		75				80
Thr	Leu	Leu	Ser	Ile	Lys	Thr	Gly	Gly	Cys	Ser	Glu	Asp	Cys	Ser	Tyr
							85			90			95		
Cys	Pro	Gln	Ser	Ser	Lys	Tyr	Asp	Thr	Gly	Val	Lys	Arg	Pro	Ser	Leu
							100			105			110		
Met	Asn	Lys	Glu	Ala	Val	Leu	Gln	Ala	Ala	Lys	Lys	Ala	Lys	Glu	Ala
							115			120			125		
Gly	Ser	Thr	Arg	Phe	Cys	Met	Gly	Ala	Ala	Trp	Arg	Asp	Thr	Leu	Gly
						130			135			140			
Arg	Lys	Thr	Asn	Phe	Asn	Gln	Ile	Leu	Glu	Tyr	Val	Lys	Asp	Ile	Arg
							145			150			155		
															160

Asp Met Gly Met Glu Val Cys Cys Thr Leu Gly Met Leu Glu Lys Gln
 165 170 175
 Gln Ala Val Glu Leu Lys Lys Ala Gly Leu Thr Ala Tyr Asn His Asn
 180 185 190
 Leu Asp Thr Ser Arg Glu Tyr Tyr Pro Asn Ile Ile Thr Thr Arg Thr
 195 200 205
 Tyr Asp Glu Arg Leu Gln Thr Leu Glu Phe Val Arg Asp Ala Gly Ile
 210 215 220
 Asn Val Cys Ser Gly Gly Ile Ile Gly Leu Gly Glu Ala Glu Glu Asp
 225 230 235 240
 Arg Val Gly Leu Leu His Thr Leu Ser Thr Leu Pro Thr His Pro Glu
 245 250 255
 Ser Val Pro Ile Asn Ala Leu Val Ala Val Lys Gly Thr Pro Leu Glu
 260 265 270
 Asp Gln Lys Pro Val Glu Ile Trp Glu Met Ile Arg Met Ile Ala Thr
 275 280 285
 Ala Arg Ile Val Met Pro Lys Ala Met Val Arg Leu Ser Ala Gly Arg
 290 295 300
 Val Arg Phe Ser Met Pro Glu Gln Ala Leu Cys Phe Leu Ala Gly Ala
 305 310 315 320
 Asn Ser Ile Phe Thr Gly Glu Lys Leu Leu Thr Thr Pro Asn Asn Asp
 325 330 335
 Phe Asp Ala Asp Gln Leu Met Phe Lys Val Leu Gly Leu Leu Pro Lys
 340 345 350
 Ala Pro Ser Leu His Glu Gly Glu Thr Ser Val Thr Glu Asp Tyr Lys
 355 360 365
 Glu Ala Ala Ser Ser Ser
 370

<210> 13
 <211> 479
 <212> DNA
 <213> Glycine max

<400> 13
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 actcgacact atctcttcct ctgttcgtct tcaagttcaa aagtgcgagaa actatggtag 120
 cgttatcatct gttccctcctc aagctacaga aacatcaagc acatcaccta gtaaggatgt 180
 ctaccaagaa gcactcaacg caactgaacc ccgcagcaat tggacaagag aagaaatcaa 240
 ggcgatctat gataagccat tgatggagtt atgttgggt gctggtagtt tgcacaggaa 300
 attccatata cctggggcta ttcaagatgt tacattgttg aacatcaaga cgggtggttg 360
 ctcggaggga ttgttcttac tggcgcccaa tcatacccgct accaaaccgg tctcaaaggc 420
 ctccaaaaat ggtcctccgt cgaatctgtc ctgcgaagcc gccccgcatac gccaaaaga 479

<210> 14
 <211> 52
 <212> PRT
 <213> Glycine max

<400> 14
 Arg Ser Asn Trp Thr Arg Glu Glu Ile Lys Ala Ile Tyr Asp Lys Pro
 1 5 10 15
 Leu Met Glu Leu Cys Trp Gly Ala Gly Ser Leu His Arg Lys Phe His
 20 25 30

Ile Pro Gly Ala Ile Gln Met Cys Thr Leu Leu Asn Ile Lys Thr Gly
35 40 45
Gly Cys Ser Glu
50

<210> 15
<211> 589
<212> DNA
<213> Triticum aestivum

<220>
<221> Unsure
<222> (321)..(321)
<223> n = A, C, G, or T

<220>
<221> Unsure
<222> (332)..(332)
<223> n = A, C, G, or T

<220>
<221> Unsure
<222> (335)..(336)
<223> n = A, C, G, or T

<220>
<221> Unsure
<222> (403)..(403)
<223> n = A, C, G, or T

<220>
<221> Unsure
<222> (407)..(407)
<223> n = A, C, G, or T

<220>
<221> Unsure
<222> (516)..(516)
<223> n = A, C, G, or T

<220>
<221> Unsure
<222> (539)..(539)
<223> n = A, C, G, or T

<220>
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<223> n = A, C, G, or T

<220>

<221> Unsure

<222> (550)..(550)

<223> n = A, C, G, or T

<220>

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<222> (555)..(555)

<223> n = A, C, G, or T

<220>

<221> Unsure

<222> (577)..(578)

<223> n = A, C, G, or T

<400> 15

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tgtcaaggac	ataagaggtt	tgggcatgga	ggctctgtgc	accctggca	tgcttagagaa	180
acaacaagct	gaagaactcc	aagaaggctg	gactttacag	cttataatca	taacctaaga	240
tacatccaag	agaatattac	ccccaaacatt	tattcctaca	agattccgtt	accgatggat	300
tagatttacc	agctcccttc	nagcatgtcc	cnnnnnaagc	tgggaattaa	ggcgccctgg	360
tcccaagggt	ggaatttatt	ggccctttt	ggagaaggcc	gnagnnaaa	cccgtttttt	420
aggctggtt	gccatacact	ggccacttt	tttgcacac	acacccaag	agagcgttcc	480
cctatccaat	gcatttgatt	gccctgtcca	aggancctc	ccttccaagg	ttttaaaanc	540
cctgttnaan	atatngaaa	ttattnccgc	atgattnncc	aacccacgg		589

<210> 16

<211> 78

<212> PRT

<213> Triticum aestivum

<220>

<221> UNSURE

<222> (69)..(69)

<223> Xaa = any amino acid

<400> 16

Asp	Ala	Val	Leu	Glu	Ala	Ala	Lys	Ala	Lys	Glu	Ala	Gly	Ser	Thr	
1				5			10						15		
Arg	Phe	Cys	Met	Gly	Ala	Ala	Trp	Arg	Glu	Thr	Ile	Gly	Arg	Lys	Thr
			20				25						30		
Asn	Phe	Asn	Gln	Ile	Leu	Glu	Tyr	Val	Lys	Asp	Ile	Arg	Gly	Met	Gly
			35			40							45		
Met	Glu	Val	Cys	Cys	Thr	Leu	Gly	Met	Leu	Glu	Lys	Gln	Gln	Ala	Glu
			50			55							60		
Glu	Leu	Gln	Glu	Xaa	Asp	Phe	Thr	Ala	Tyr	Asn	His	Asn	Leu		
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<210> 17
 <211> 1396
 <212> DNA
 <213> Hordeum vulgare

<400> 17

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cccccttcgc	ctccggcggt	agcggccgc	ccttctcatc	ggtatcgccg	ggcgccggcg	180
aggcggagcg	ggcgtgtccg	gacggggcca	ggaacgactg	gacccccc	gagatccagg	240
ccatctacga	ctccccgctc	ctcgacccctc	tcttccacgg	ggctcaagtc	cataggaatg	300
tccataaaatt	tagagaagtg	caacaatgca	cacttcttca	aataaagact	ggtgggtgca	360
gccaagatgtt	ttcatactgc	ccacagtctt	caagatacag	taccggattt	aaggctgaaa	420
aattaatgaa	gaaagatgcc	gtcctagaag	cagctaaaaa	ggcaaaaggag	gctgggagca	480
cccgattttt	catgggagcc	gcatggagag	agacaatttg	caggaaaaca	aacttcaacc	540
agattcttga	atatgtcaag	gacataagag	gtatggcat	ggaggtctgt	tgcaccctgg	600
gcatgctaga	gaaacagcaa	gctgaagaac	tcaagaaggc	tggacttaca	gcttataatc	660
ataacctaga	tacatcaaga	aatattacc	cgaacattat	ttctacaaga	tcgtatgtatg	720
atagattaca	gactcttcag	catgtccgtg	aagctggaaat	aagcgtctgc	tcaaggatggaa	780
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tgccaacaca	cccagagagt	gttcctatca	atgcattgtat	tgctgtcaaa	ggcacgcctc	900
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ccaaggcacc	gaaccttggc	gatgaggagg	ccaccgtggc	atcatccacg	gagagatgtg	1200
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ctggcaccat	tatctccagc	tagagcttt	tactgttaggg	atcatgatat	tttgtactcc	1320
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<210> 18
 <211> 405
 <212> PRT
 <213> Hordeum vulgare

<400> 18

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									20	25					30	
Ser	Leu	Arg	Ser	Arg	Val	Arg	Ser	Pro	Phe	Ala	Ser	Ala	Val	Ser	Ala	
									35	40					45	
Ala	Pro	Phe	Ser	Ser	Val	Ser	Ala	Ala	Ala	Ala	Glu	Ala	Glu	Arg	Ala	
							50		55		60					
Val	Arg	Asp	Gly	Pro	Arg	Asn	Asp	Trp	Thr	Arg	Pro	Glu	Ile	Gln	Ala	
								65	70		75				80	
Ile	Tyr	Asp	Ser	Pro	Leu	Leu	Asp	Leu	Leu	Phe	His	Gly	Ala	Gln	Val	
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His	Arg	Asn	Val	His	Lys	Phe	Arg	Glu	Val	Gln	Gln	Cys	Thr	Leu	Leu	
								100		105					110	
Ser	Ile	Lys	Thr	Gly	Gly	Cys	Ser	Glu	Asp	Cys	Ser	Tyr	Cys	Pro	Gln	
							115		120						125	

Ser Ser Arg Tyr Ser Thr Gly Leu Lys Ala Glu Lys Leu Met Lys Lys
 130 135 140
 Asp Ala Val Leu Glu Ala Ala Lys Lys Ala Lys Glu Ala Gly Ser Thr
 145 150 155 160
 Arg Phe Cys Met Gly Ala Ala Trp Arg Glu Thr Ile Gly Arg Lys Thr
 165 170 175
 Asn Phe Asn Gln Ile Leu Glu Tyr Val Lys Asp Ile Arg Gly Met Gly
 180 185 190
 Met Glu Val Cys Cys Thr Leu Gly Met Leu Glu Lys Gln Gln Ala Glu
 195 200 205
 Glu Leu Lys Lys Ala Gly Leu Thr Ala Tyr Asn His Asn Leu Asp Thr
 210 215 220
 Ser Arg Glu Tyr Tyr Pro Asn Ile Ile Ser Thr Arg Ser Tyr Asp Asp
 225 230 235 240
 Arg Leu Gln Thr Leu Gln His Val Arg Glu Ala Gly Ile Ser Val Cys
 245 250 255
 Ser Gly Gly Ile Ile Gly Leu Gly Glu Ala Glu Glu Asp Arg Val Gly
 260 265 270
 Leu Leu His Thr Leu Ala Thr Leu Pro Thr His Pro Glu Ser Val Pro
 275 280 285
 Ile Asn Ala Leu Ile Ala Val Lys Gly Thr Pro Leu Gln Asp Gln Lys
 290 295 300
 Pro Val Glu Ile Trp Glu Met Ile Arg Met Ile Ala Ser Ala Arg Ile
 305 310 315 320
 Val Met Pro Lys Ala Met Val Arg Leu Ser Ala Gly Arg Val Arg Phe
 325 330 335
 Ser Met Pro Glu Gln Ala Leu Cys Phe Leu Ala Gly Ala Asn Ser Ile
 340 345 350
 Phe Ala Gly Glu Lys Leu Leu Thr Thr Ala Asn Asn Asp Phe Asp Ala
 355 360 365
 Asp Gln Ala Met Phe Lys Ile Leu Gly Leu Ile Pro Lys Ala Pro Asn
 370 375 380
 Phe Gly Asp Glu Glu Ala Thr Val Ala Ser Ser Thr Glu Arg Cys Glu
 385 390 395 400
 Gln Ala Ala Ser Met
 405

<210> 19
 <211> 1467
 <212> DNA
 <213> Zea mays

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 cgcccgctgc tcctctatcc ctccctgtct gctgtacta ccttaagcta tcaactatcat 180
 ggccttgatg ctgttagcgc gcaacctgctg cttccgcctc cggccaccgc tcgcccggc 240
 cgcggcggttc tcgtcgcccg cggcggaggc ggagagggcg atacgggacg ggccggggaa 300
 cgactggagc cggccccgaga tccaggccgt ctacgactca ccgcctctcg acctccttt 360
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 atatgctgtc ttggaaagcag caaaaaaggc aaaagagtct gggagcaccc gtttttgcat 480
 gggagctgca tggagagaaa ccattggcag gaaatcaaac ttcaaccaga ttcttgaata 540
 tgtcaaggaa ataagggtta tggcatgga ggtctgttgc acactaggca tgatagagaa 600
 acaacaagct gaagaactca agaaggctgg attacagca tataatcata accttagatac 660
 atcaagagag tattatccca acattattac cacaagatca tatgatgata gactgcagac 720

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gcctgttagag	atctggaaa	tgatccgcat	gatcgccact	gctcgatca	cgatgccaaa	960
ggcaatgggt	aggcttcag	caggccgagt	acggttctcg	atgccagaac	aagcgctgtg	1020
cttcctcgct	ggggccaaact	ccatcttgc	cggcgagaaa	cttctcacaa	ccgcaaaca	1080
cgactttgat	gcccggaccagg	cgatgttcaa	gatccttggc	ctgatcccc	aggctccaag	1140
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tgcttcgatg	tagaatatat	acatatcatt	accgattatc	cgtatcacgg	ttggggcgaa	1260
actagaacta	ccgttgtagc	tagagcattt	gattgtagaa	accacaacat	ttcattattt	1320
tgtaattgct	tgagactgaa	tggggatac	ccatgtcggg	ctagatcaat	ggacaacttc	1380
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<210> 20
<211> 344
<212> PRT
<213> Zea mays

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20	25	30				
Arg Ala Ile Arg Asp Gly	Pro Arg Asn Asp	Trp Ser Arg	Pro Glu Ile			
35	40	45				
Gln Ala Val Tyr Asp Ser	Pro Leu Leu Asp	Leu Leu Phe	His Gly Ala			
50	55	60				
Gln Ser Ser Arg Tyr Asn	Thr Gly Leu Lys	Ala Gln Lys	Leu Met Asn			
65	70	75	80			
Lys Tyr Ala Val Leu	Glu Ala Ala Lys	Lys Ala Lys	Glu Ser Gly Ser			
85	90	95				
Thr Arg Phe Cys Met	Gly Ala Ala Trp	Arg Glu Thr Ile	Gly Arg Lys			
100	105	110				
Ser Asn Phe Asn Gln Ile	Leu Glu Tyr Val	Lys Glu Ile	Arg Gly Met			
115	120	125				
Gly Met Glu Val Cys Cys	Thr Leu Gly Met	Ile Glu Lys	Gln Gln Ala			
130	135	140				
Glu Glu Leu Lys Lys	Ala Gly Leu Thr	Ala Tyr Asn His	Asn Leu Asp			
145	150	155	160			
Thr Ser Arg Glu Tyr	Tyr Pro Asn Ile	Ile Thr Thr Arg	Ser Tyr Asp			
165	170	175				
Asp Arg Leu Gln Thr	Leu Glu His Val	Arg Glu Ala Gly	Ile Ser Ile			
180	185	190				
Cys Ser Gly Gly Ile	Ile Gly Leu Gly	Glu Ala Glu	Glu Asp Arg Val			
195	200	205				
Gly Leu Leu His Thr	Leu Ala Thr Leu	Pro Thr His	Pro Glu Ser Val			
210	215	220				
Pro Ile Asn Ala Leu	Val Ala Val Lys	Gly Thr Pro	Leu Glu Asp Gln			
225	230	235	240			
Lys Pro Val Glu Ile	Trp Glu Met Ile	Arg Met Ile	Ala Thr Ala Arg			
245	250	255				
Ile Thr Met Pro Lys Ala	Met Val Arg	Leu Ser Ala Gly	Arg Val Arg			
260	265	270				
Phe Ser Met Pro Glu	Gln Ala Leu Cys	Phe Leu Ala Gly	Ala Asn Ser			

275	280	285	
Ile Phe Ala Gly Glu Lys Leu	Leu Thr Thr Ala Asn	Asn Asp Phe Asp	
290	295	300	
Ala Asp Gln Ala Met Phe Lys Ile	Leu Gly Leu Ile Pro Lys Ala Pro		
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Arg Ser Glu Gln Ala Ala Ser Met			
	340		

<210> 21
<211> 1515
<212> DNA
<213> Zea mays

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gctcgccgcc	gccgcggcg	tctcgccg	cgcggcgag	gcggagaggg	cgatacggga	240
cggggcccg	aacgactgga	gccggcccga	gatccagggc	gtctacgact	caccgctcct	300
cgaccccttc	tttcacgggg	ctcagggtcca	cagaaatgtc	cataaaattca	gagaagtgc	360
gcaatgcaca	cttctttcaa	tcaagactgg	tggatgcagt	gaagattgtt	cttactgtcc	420
tcagtcata	agataacaaca	ctggattgaa	ggcccaaaaa	tttatgaaca	aagatgtgt	480
cttggaaagca	gcaaaaaagg	caaaagagtc	tgggagcacc	cgttttgca	tgggagctgc	540
atggagagaa	accattggca	ggaaatcaaa	cttcaaccag	attcttgaat	atgtcaagga	600
aataaggggt	atgggcatgg	aggtctgttgc	cacactagggc	atgatagaga	aacaacaagg	660
tgaagaactc	aagaaggctg	gacttacagc	atataatcat	aacctagata	catcaagaga	720
gtattatccc	aacattatta	ccacaagatc	atatgtat	agactgcaga	ctcttgagca	780
tgtccgtgaa	gctggataaa	gcatctgctc	aggtggatc	attggctttg	gtgaagcaga	840
ggaggaccgg	gtagggttgt	tgcataccct	agctaccttgc	cctacacacc	cagagagcgt	900
tccttattaa	gcattggttg	ctgtaaaagg	cacacccctt	gaggaccaga	agcctgtaga	960
gatctggaa	atgatccgca	tgatcgccac	tgctcggtac	acgatgcca	aggcaatgg	1020
gaggcttca	gcaggccgag	tacggttctc	gatgccagaa	caagcgtgt	gcttcctcgc	1080
tggggccaac	tccatctttg	ccggcgagaa	acttctcaca	accgcaaaca	acgactttga	1140
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ggaagaggtg	tctgcggcg	ctcccgca	atccgagagg	tctgagcaag	ctgcttcgt	1260
gtagaatata	tacatatcat	taccgattat	ccgtatcacg	gttggggcga	aactagaact	1320
accgttgtag	ctagagcatt	ggattgtaga	aaccacaaaca	tttcattatt	ttgtattgc	1380
ttgagactga	atgggggata	cccatgtcg	gctagatcaa	aaaaaaaaaa	aaaaaaaaaa	1440
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aaaaaaaaaa	aaaaaa					1515

<210> 22
<211> 377
<212> PRT
<213> Zea mays

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<400> 22
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5 . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . .
10 . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . .
15 . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . .
Pro Leu Ala Ala Ala Ala Ala Phe Ser Ser Ala Ala Ala Glu Ala Glu
20 . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . .
25 . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . .
30 . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . .
Arg Ala Ile Arg Asp Gly Pro Arg Asn Asp Trp Ser Arg Pro Glu Ile

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35	40	45
Gln Ala Val Tyr Asp Ser Pro	Leu Leu Asp	Leu Phe His Gly Ala
50	55	60
Gln Val His Arg Asn Val His	Lys Phe Arg	Glu Val Gln Gln Cys Thr
65	70	75
Leu Leu Ser Ile Lys Thr Gly	Gly Cys Ser	Glu Asp Cys Ser Tyr Cys
85	90	95
Pro Gln Ser Ser Arg Tyr Asn Thr	Gly Leu Lys	Ala Gln Lys Leu Met
100	105	110
Asn Lys Asp Ala Val Leu Glu	Ala Ala Lys	Lys Ala Lys Glu Ser Gly
115	120	125
Ser Thr Arg Phe Cys Met	Gly Ala Ala	Trp Arg Glu Thr Ile Gly Arg
130	135	140
Lys Ser Asn Phe Asn Gln Ile	Leu Glu Tyr	Val Lys Glu Ile Arg Gly
145	150	155
Met Gly Met Glu Val Cys Cys	Thr Leu Gly	Met Ile Glu Lys Gln Gln
165	170	175
Ala Glu Glu Leu Lys Lys	Ala Gly Leu	Thr Ala Tyr Asn His Asn Leu
180	185	190
Asp Thr Ser Arg Glu Tyr Tyr	Pro Asn Ile Ile	Thr Thr Arg Ser Tyr
195	200	205
Asp Asp Arg Leu Gln Thr	Leu Glu His Val Arg	Glu Ala Gly Ile Ser
210	215	220
Ile Cys Ser Gly Gly	Ile Ile Gly Leu	Gly Glu Ala Glu Glu Asp Arg
225	230	235
Val Gly Leu Leu His Thr	Leu Ala Thr	Leu Pro Thr His Pro Glu Ser
245	250	255
Val Pro Ile Asn Ala Leu Val	Ala Val Lys	Gly Thr Pro Leu Glu Asp
260	265	270
Gln Lys Pro Val Glu Ile Trp	Glu Met Ile Arg	Met Ile Ala Thr Ala
275	280	285
Arg Ile Thr Met Pro Lys	Ala Met Val Arg	Leu Ser Ala Gly Arg Val
290	295	300
Arg Phe Ser Met Pro Glu	Gln Ala Leu Cys	Phe Leu Ala Gly Ala Asn
305	310	315
Ser Ile Phe Ala Gly Glu	Lys Leu Leu	Thr Thr Ala Asn Asn Asp Phe
325	330	335
Asp Ala Asp Gln Ala Met Phe	Lys Ile Leu	Gly Leu Ile Pro Lys Ala
340	345	350
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Glu Arg Ser Glu Gln Ala	Ala Ser Met	
370	375	

<210> 23
 <211> 1439
 <212> DNA
 <213> Zea mays

<400> 23
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 ttgatgctgc tagcgcgcaa cctgcgcgtcc cgccctccgccc caccgcgtcgc cgccgcgcg 180
 gcgttctcgt cggccgcggc ggaggcggag agggcgatac gggacgggcc gcggaacgac 240
 tggagccggc ccgagatcca ggccgtctac gactcaccgc tcctcgaccc cctctttcac 300

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aacactggat	tgaaggccca	aaaattgtat	aacaatatg	ctgtcttggaa	agcagcaaaa	480
aaggcaaaag	agtctggag	caccgtttt	tgcattggag	ctgcattggag	agaaaccatt	540
ggcagggaaat	caaactcaa	ccagattctt	gaatatgtca	aggaaataag	gggtatggc	600
atggaggtct	gttgcacact	aggcatgata	gagaaacaac	aagctgaaga	actcaagaag	660
gctggactta	cagcatataa	tcataaccta	gatacatcaa	gagagtatta	tcccaacatt	720
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ttgttgcatc	ccctagctac	cttgccatac	caccagaga	gcgttcttat	taatgcattg	900
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cgagtacggt	tctcgatgcc	agaacaagcg	ctgtgcttcc	tcgctgggc	caactccatc	1080
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tcattaccga	ttatccgtat	cacgggttggg	gcgaaactag	aactaccgtt	gtagctagag	1320
cattggatg	tagaaaccac	aacatttcat	tatttgtaa	ttgcttgaga	ctgaatgggg	1380
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<210> 24
<211> 377
<212> PRT
<213> Zea mays

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Arg Ala Ile Arg Asp Gly Pro Arg Asn Asp Trp Ser Arg	Pro Glu Ile					
35	40	45				
Gln Ala Val Tyr Asp Ser Pro Leu Leu Asp Leu Leu Phe	His Gly Ala					
50	55	60				
Gln Val His Arg Asn Val His Lys Phe Arg Glu Val Gln	Gln Cys Thr					
65	70	75	80			
Leu Leu Ser Ile Lys Thr Gly Gly Cys Ser Glu Asp Cys	Ser Tyr Cys					
85	90	95				
Pro Gln Ser Ser Arg Tyr Asn Thr Gly Leu Lys Ala Gln	Lys Leu Met					
100	105	110				
Asn Lys Tyr Ala Val Leu Glu Ala Ala Lys Lys Ala Lys	Glu Ser Gly					
115	120	125				
Ser Thr Arg Phe Cys Met Gly Ala Ala Trp Arg Glu Thr	Ile Gly Arg					
130	135	140				
Lys Ser Asn Phe Asn Gln Ile Leu Glu Tyr Val Lys Glu	Ile Arg Gly					
145	150	155	160			
Met Gly Met Glu Val Cys Cys Thr Leu Gly Met Ile Glu	Lys Gln Gln					
165	170	175				
Ala Glu Glu Leu Lys Lys Ala Gly Leu Thr Ala Tyr Asn	His Asn Leu					
180	185	190				
Asp Thr Ser Arg Glu Tyr Tyr Pro Asn Ile Ile Thr Thr	Arg Ser Tyr					
195	200	205				
Asp Asp Arg Leu Gln Thr Leu Glu His Val Arg Glu Ala	Gly Ile Ser					
210	215	220				
Ile Cys Ser Gly Gly Ile Ile Gly Leu Gly Glu Ala Glu	Glu Asp Arg					

225	230	235	240												
Val	Gly	Leu	Leu	His	Thr	Leu	Ala	Thr	Leu	Pro	Thr	His	Pro	Glu	Ser
		245				250								255	
Val	Pro	Ile	Asn	Ala	Leu	Val	Ala	Val	Lys	Gly	Thr	Pro	Leu	Glu	Asp
		260				265								270	
Gln	Lys	Pro	Val	Glu	Ile	Trp	Glu	Met	Ile	Arg	Met	Ile	Ala	Thr	Ala
														285	
		275				280									
Arg	Ile	Thr	Met	Pro	Lys	Ala	Met	Val	Arg	Leu	Ser	Ala	Gly	Arg	Val
		290				295							300		
Arg	Phe	Ser	Met	Pro	Glu	Gln	Ala	Leu	Cys	Phe	Leu	Ala	Gly	Ala	Asn
														320	
		305				310						315			
Ser	Ile	Phe	Ala	Gly	Glu	Lys	Leu	Leu	Thr	Thr	Ala	Asn	Asn	Asp	Phe
														335	
		325										330			
Asp	Ala	Asp	Gln	Ala	Met	Phe	Lys	Ile	Leu	Gly	Leu	Ile	Pro	Lys	Ala
														350	
		340										345			
Pro	Ser	Phe	Gly	Glu	Glu	Glu	Ala	Ser	Ala	Ala	Ala	Pro	Thr	Glu	Ser
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		355										360			
Glu	Arg	Ser	Glu	Gln	Ala	Ala	Ser	Met							
		370										375			

<210> 25
<211> 1477
<212> DNA
<213> Argemone mexicana

<400> 25															
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aatctttag	agctcgctt	cgacccttga	tttcatttc	tacatttct	tctctctcat										180
catcttcttc	ttcttcagct	gctgctgttc	aagcagaaag	aacgattaaa	gaagggtccaa										240
gaaacgatg	gagcagagat	gaaattaaat	cggtttatga	ttcttcagtt	ctcgatcttc										300
tcttccatgc	agctcaagtc	catagacatg	ctcacaactt	cagggaaatg	cagcaatgt										360
ctcttcttc	tgttaagaca	ggtggttgca	gtgaagattt	ttcatattgt	ccacaatctt										420
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aaggcaggat	caatgtctgc	tcaggaggaa	taatagggt	aggagaagca	gaggaggatc										840
gagttggct	tttgcataca	ctagcaacgc	ttcccttcaca	tccagaaaatg	ttccatccatca										900
atgcattgt	tgcagtcaaa	ggcacaccc	ttgaagatca	gaagccagtt	gaaatatggg										960
agatgattcg	gatgattgt	actgctagaa	ttgtaatgcc	aaaagcaatg	gtcaggctat										1020
cagcaggatcg	tgttcgat	tccatgtccg	agcaagctt	ctgcttcctt	gctggcgcca										1080
attccatctt	cactggtgag	aaactattga	caactccaa	caatgatttt	gacgcagatc										1140
aaatgtatgtt	taagatttt	gggctgacac	caaaaagctcc	aaattttgc	caaacatcaa										1200
catcttgcga	agccgagaga	tgtgaacaag	aagcaactgc	gtcatagttc	ttgttgcgtat										1260
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aaaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa										1477

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<211> 379

<212> PRT
<213> Argemone mexicana

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35 40 45
Ser Arg Asp Glu Ile Lys Ser Val Tyr Asp Ser Pro Val Leu Asp Leu
50 55 60
Leu Phe His Ala Ala Gln Val His Arg His Ala His Asn Phe Arg Glu
65 70 75 80
Val Gln Gln Cys Thr Leu Leu Ser Val Lys Thr Gly Gly Cys Ser Glu
85 90 95
Asp Cys Ser Tyr Cys Pro Gln Ser Ser Arg Tyr Asp Thr Gly Val Lys
100 105 110
Ala Gln Lys Leu Met Asn Lys Asp Ala Val Leu Gln Ala Ala Glu Lys
115 120 125
Ala Lys Glu Ala Gly Ser Thr Arg Phe Cys Met Gly Ala Ala Trp Arg
130 135 140
Asp Thr Val Gly Arg Lys Thr Asn Phe Lys Gln Ile Leu Glu Tyr Val
145 150 155 160
Lys Glu Ile Arg Gly Met Gly Met Glu Val Cys Cys Thr Leu Gly Met
165 170 175
Ile Glu Lys Gln Gln Ala Val Glu Leu Lys Gln Ala Gly Leu Thr Ala
180 185 190
Tyr Asn His Asn Leu Asp Thr Ser Arg Glu Tyr Tyr Pro Asn Ile Ile
195 200 205
Thr Thr Arg Ser Tyr Asp Glu Arg Leu Glu Thr Leu Gln Phe Val Arg
210 215 220
Glu Ala Gly Ile Asn Val Cys Ser Gly Gly Ile Ile Gly Leu Gly Glu
225 230 235 240
Ala Glu Glu Asp Arg Val Gly Leu Leu His Thr Leu Ala Thr Leu Pro
245 250 255
Ser His Pro Glu Ser Val Pro Ile Asn Ala Leu Leu Ala Val Lys Gly
260 265 270
Thr Pro Leu Glu Asp Gln Lys Pro Val Glu Ile Trp Glu Met Ile Arg
275 280 285
Met Ile Ala Thr Ala Arg Ile Val Met Pro Lys Ala Met Val Arg Leu
290 295 300
Ser Ala Gly Arg Val Arg Phe Ser Met Ser Glu Gln Ala Leu Cys Phe
305 310 315 320
Leu Ala Gly Ala Asn Ser Ile Phe Thr Gly Glu Lys Leu Leu Thr Thr
325 330 335
Pro Asn Asn Asp Phe Asp Ala Asp Gln Met Met Phe Lys Ile Leu Gly
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<210> 27
<211> 1526



<212> DNA
 <213> Glycine max

<400> 27

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aaataccgtt	gttgtctgtt	gtctctgtcg	tgtctatatt	cgcagatctc	tcactcatc	180
tctgttgtt	ctctgc当地	cttcgaattc	gaaagcaaaa	acatgtttt	ggcgagaccc	240
atttcccgag	caccctccct	tttggcggtt	cactcttct	acgcgtattc	ctctgc当地	300
gcagctgcaa	ttcaagctga	gagagccatc	aaagaaggac	ccagaaacga	ttggagccga	360
gaccaagtca	aatccatcta	cgactctccc	attctcgatc	ttcttcca	tggggctcaa	420
gttcacagac	atgtcataa	cttcaggaa	gttcagcagt	gtacttct	gtctatcaa	480
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gtcaaaggcc	aacgccttat	gaacaaggaa	gctgttctac	aggctcaaa	gaaggcaaaa	600
gaggctggg	gcactcgctt	ttgtatgggt	gctgcatgga	gggatacact	ggaaagaaaag	660
accaactca	accagatct	tgaatatgt	aaagacataa	gggacatggg	aatggaggtt	720
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actgcctata	atcacaatct	tgacacttca	aggagtatt	atccaaacat	catcacaaca	840
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acattgtcaa	cactcccac	ccatccagag	agtgtccata	ttaatgcact	tgttgc当地	1020
aagggAACCC	ctcttgagga	tcagaagct	gttggaaat	gggagatgt	tcgcatgata	1080
gcaactgcac	gtatcgtaat	gccaaaagca	atggtcaggt	tatcagctgg	cagagttcga	1140
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aaaaagctc	tcactactcc	taacaatgt	tttgc当地	atcaactcat	gtttaaagg	1260
cttggacttc	tccaaaagc	tccaaagctt	catgaagg	aaactagtgt	gacagaagat	1320
tataaggaa	cagtttcttc	tagttgagtt	gtcaacgg	tcaaaacaat	atctgtgatc	1380
cttcaacttc	tctaattgt	cattagcatg	tactgatgtt	aggttcatt	gaatttgct	1440
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<210> 28

<211> 415

<212> PRT

<213> Glycine max

<400> 28

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						20		25						30	
Pro	Asn	Phe	Glu	Phe	Glu	Ser	Lys	Asn	Met	Phe	Leu	Ala	Arg	Pro	Ile
						35		40						45	
Phe	Arg	Ala	Pro	Ser	Leu	Trp	Ala	Leu	His	Ser	Ser	Tyr	Ala	Tyr	Ser
						50		55				60			
Ser	Ala	Ser	Ala	Ala	Ala	Ile	Gln	Ala	Glu	Arg	Ala	Ile	Lys	Glu	Gly
						65		70				75		80	
Pro	Arg	Asn	Asp	Trp	Ser	Arg	Asp	Gln	Val	Lys	Ser	Ile	Tyr	Asp	Ser
						85		90						95	
Pro	Ile	Leu	Asp	Leu	Leu	Phe	His	Gly	Ala	Gln	Val	His	Arg	His	Ala
						100		105						110	
His	Asn	Phe	Arg	Glu	Val	Gln	Gln	Cys	Thr	Leu	Leu	Ser	Ile	Lys	Thr
						115		120						125	
Gly	Gly	Cys	Ser	Glu	Asp	Cys	Ser	Tyr	Cys	Pro	Gln	Ser	Ser	Lys	Tyr
						130		135						140	

Asp	Thr	Gly	Val	Lys	Gly	Gln	Arg	Leu	Met	Asn	Lys	Glu	Ala	Val	Leu
145				150						155					160
Gln	Ala	Ala	Lys	Lys	Ala	Lys	Glu	Ala	Gly	Ser	Thr	Arg	Phe	Cys	Met
				165					170					175	
Gly	Ala	Ala	Trp	Arg	Asp	Thr	Leu	Gly	Arg	Lys	Thr	Asn	Phe	Asn	Gln
			180				185						190		
Ile	Leu	Glu	Tyr	Val	Lys	Asp	Ile	Arg	Asp	Met	Gly	Met	Glu	Val	Cys
		195					200					205			
Cys	Thr	Leu	Gly	Met	Leu	Glu	Lys	Gln	Gln	Ala	Val	Glu	Leu	Lys	Lys
	210				215					220					
Ala	Gly	Leu	Thr	Ala	Tyr	Asn	His	Asn	Leu	Asp	Thr	Ser	Arg	Glu	Tyr
225				230						235					240
Tyr	Pro	Asn	Ile	Ile	Thr	Thr	Arg	Thr	Tyr	Asp	Glu	Arg	Leu	Gln	Thr
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Leu	Glu	Phe	Val	Arg	Asp	Ala	Gly	Ile	Asn	Val	Cys	Ser	Gly	Gly	Ile
		260				265					270				
Ile	Gly	Leu	Gly	Glu	Ala	Glu	Glu	Asp	Arg	Val	Gly	Leu	Leu	His	Thr
	275				280						285				
Leu	Ser	Thr	Leu	Pro	Thr	His	Pro	Glu	Ser	Val	Pro	Ile	Asn	Ala	Leu
	290				295						300				
Val	Ala	Val	Lys	Gly	Thr	Pro	Leu	Glu	Asp	Gln	Lys	Pro	Val	Glu	Ile
305				310						315					320
Trp	Glu	Met	Ile	Arg	Met	Ile	Ala	Thr	Ala	Arg	Ile	Val	Met	Pro	Lys
				325				330					335		
Ala	Met	Val	Arg	Leu	Ser	Ala	Gly	Arg	Val	Arg	Phe	Ser	Met	Pro	Glu
			340				345					350			
Gln	Ala	Leu	Cys	Phe	Leu	Ala	Gly	Ala	Asn	Ser	Ile	Phe	Thr	Gly	Glu
		355				360					365				
Lys	Leu	Leu	Thr	Thr	Pro	Asn	Asn	Asp	Phe	Asp	Ala	Asp	Gln	Leu	Met
	370				375					380					
Phe	Lys	Val	Leu	Gly	Leu	Leu	Pro	Lys	Ala	Pro	Ser	Leu	His	Glu	Gly
385				390						395					400
Glu	Thr	Ser	Val	Thr	Glu	Asp	Tyr	Lys	Glu	Ala	Ala	Ser	Ser	Ser	
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<210> 29  
<211> 1659  
<212> DNA  
<213> Glycine max
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taaaaccatc	gtgcgttgg	cagctggaa	aggagaatt	agcgaggaac	aacaggtctt	1080
atgtttcatg	gccggagcca	atgccgttt	cacaggagaa	acaatgtta	ccacaccagc	1140
cgttggatgg	ggtgtcgatt	ccgtcgttt	caacagatgg	ggattaagac	ccatggaaag	1200
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cccagggcgt	tttgtcgcgt	catcatctcg	agtttttgc	aggagattcg	aacagtggaa	1380
gtgccgttgc	gcaccattt	ggattggcgt	atcggactga	gattgactgt	gccacgaaaa	1440
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ggttttgttt	gatgtgagag	aatgattgtt	tagaagggg	gaatgtatat	acggaacagt	1560
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aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa			1659

<210> 30
<211> 417
<212> PRT
<213> Glycine max

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 35 40 45
 Ala Thr Glu Thr Ser Ser Thr Ser Pro Ser Lys Asp Val Tyr Gln Glu
 50 55 60
 Ala Leu Asn Ala Thr Glu Pro Arg Ser Asn Trp Thr Arg Glu Glu Ile
 65 70 75 80
 Lys Ala Ile Tyr Asp Lys Pro Leu Met Glu Leu Cys Trp Gly Ala Gly
 85 90 95
 Ser Leu His Arg Lys Phe His Ile Pro Gly Ala Ile Gln Met Cys Thr
 100 105 110
 Leu Leu Asn Ile Lys Thr Gly Gly Cys Ser Glu Asp Cys Ser Tyr Cys
 115 120 125
 Ala Gln Ser Ser Arg Tyr Gln Thr Gly Leu Lys Ala Ser Lys Met Val
 130 135 140
 Ser Val Glu Ser Val Leu Ala Ala Ala Arg Ile Ala Lys Asp Asn Gly
 145 150 155 160
 Ser Thr Arg Phe Cys Met Gly Ala Ala Trp Arg Asp Met Arg Gly Arg
 165 170 175
 Lys Thr Asn Leu Lys Asn Val Lys Thr Met Val Ser Glu Ile Arg Gly
 180 185 190
 Met Gly Met Glu Val Cys Val Thr Leu Gly Met Ile Asp Ala Glu Gln
 195 200 205
 Ala Gln Glu Leu Lys Glu Ala Gly Leu Thr Ala Tyr Asn His Asn Val
 210 215 220
 Asp Thr Ser Arg Asp Phe Tyr Pro Lys Val Ile Thr Thr Arg Thr Tyr
 225 230 235 240
 Asp Glu Arg Leu Asp Thr Ile Lys Asn Val Arg Glu Ala Gly Ile Asn
 245 250 255
 Val Cys Thr Gly Gly Ile Leu Gly Leu Gly Glu Asn Lys Ser Asp His
 260 265 270

Ile Gly Leu Leu Glu Thr Val Ala Thr Leu Pro Ser His Pro Glu Ser
 275 280 285
 Phe Pro Val Asn Met Leu Val Ala Ile Lys Gly Thr Pro Leu Glu Gly
 290 295 300
 Asn Lys Lys Val Glu Phe Glu Asn Met Leu Arg Met Val Ala Thr Ala
 305 310 315 320
 Arg Ile Val Met Pro Lys Thr Ile Val Arg Leu Ala Ala Gly Arg Gly
 325 330 335
 Glu Leu Ser Glu Glu Gln Gln Val Leu Cys Phe Met Ala Gly Ala Asn
 340 345 350
 Ala Val Phe Thr Gly Glu Thr Met Leu Thr Thr Pro Ala Val Gly Trp
 355 360 365
 Gly Val Asp Ser Val Val Phe Asn Arg Trp Gly Leu Arg Pro Met Glu
 370 375 380
 Ser Phe Glu Val Glu Ala Leu Lys Asn Asp Lys Pro Ala Thr Thr Asn
 385 390 395 400
 Thr Glu Ile Pro Val Glu Ala Ser Lys Ala Glu Met Pro Gly Thr Val
 405 410 415
 Ala

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<210> 31
 <211> 1032
 <212> DNA
 <213> Triticum aestivum

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 ttgaatatgt caaggacata agaggtatgg gcatggaggt ctgttgcacc ctgggcattgc 180
 tagagaaaaca acaagctgaa gaactcaaga aggctggact tacagcttat aatcataacc 240
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 tacagactct tcagcatgtc cgtgaagctg gaataagcgt ctgctcaggta gaaattattg 360
 gtcttgaga ggcggaggaa gaccgtgttag ggctgttgcatacactggcc actttgc当地 420
 cacacccaga gagcgttct atcaatgcat tgattgtgt caaaggcact ccttgc当地 480
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 ctctctgtt tctcgctggg gccaactcga tcttcgccc当地 tgaaaagctc ctgacaactg 660
 cgaacaatga ctttgatgc当地 gaccaggcaa tggtaagat ctttgc当地 attcccaagg 720
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1020
 aaaaaaaaaa aa 1032

<210> 32
 <211> 263
 <212> PRT
 <213> Triticum aestivum

<400> 32
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植物学报

Ser Thr Arg Phe Cys Met Gly Ala Ala Trp Arg Glu Thr Ile Gly Arg
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 Lys Thr Asn Phe Asn Gln Ile Leu Glu Tyr Val Lys Asp Ile Arg Gly
 35 40 45
 Met Gly Met Glu Val Cys Cys Thr Leu Gly Met Leu Glu Lys Gln Gln
 50 55 60
 Ala Glu Glu Leu Lys Lys Ala Gly Leu Thr Ala Tyr Asn His Asn Leu
 65 70 75 80
 Asp Thr Ser Arg Glu Tyr Tyr Pro Asn Ile Ile Ser Thr Arg Ser Tyr
 85 90 95
 Asp Asp Arg Leu Gln Thr Leu Gln His Val Arg Glu Ala Gly Ile Ser
 100 105 110
 Val Cys Ser Gly Gly Ile Ile Gly Leu Gly Glu Ala Glu Glu Asp Arg
 115 120 125
 Val Gly Leu Leu His Thr Leu Ala Thr Leu Pro Thr His Pro Glu Ser
 130 135 140
 Val Pro Ile Asn Ala Leu Ile Ala Val Lys Gly Thr Pro Leu Gln Asp
 145 150 155 160
 Gln Lys Pro Val Glu Ile Trp Glu Met Ile Arg Met Ile Ala Ser Ala
 165 170 175
 Arg Ile Val Met Pro Lys Ala Met Val Arg Leu Ser Ala Gly Arg Val
 180 185 190
 Arg Phe Ser Met Pro Glu Gln Ala Leu Cys Phe Leu Ala Gly Ala Asn
 195 200 205
 Ser Ile Phe Ala Gly Glu Lys Leu Leu Thr Thr Ala Asn Asn Asp Phe
 210 215 220
 Asp Ala Asp Gln Ala Met Phe Lys Ile Leu Gly Leu Ile Pro Lys Ala
 225 230 235 240
 Pro Asn Phe Gly Asp Glu Glu Val Met Val Ala Ala Pro Thr Glu Arg
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 Cys Glu Gln Ala Ala Leu Met
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<210> 33
 <211> 378
 <212> PRT
 <213> Arabidopsis thaliana

<400> 33

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Ser	Ala	Glu	Ala	Glu	Arg	Thr	Ile	Arg	Glu	Gly	Pro	Arg	Asn	Asp	Trp	45
Ser	Arg	Asp	Glu	Ile	Lys	Ser	Val	Tyr	Asp	Ser	Pro	Leu	Leu	Asp	Leu	60
Leu	Phe	His	Gly	Ala	Gln	Val	His	Arg	His	Val	His	Asn	Phe	Arg	Glu	80
65																
Val	Gln	Gln	Cys	Thr	Leu	Leu	Ser	Ile	Lys	Thr	Gly	Gly	Cys	Ser	Glu	95
Asp	Cys	Ser	Tyr	Cys	Pro	Gln	Ser	Ser	Arg	Tyr	Ser	Thr	Gly	Val	Lys	110
Ala	Gln	Arg	Leu	Met	Ser	Lys	Asp	Ala	Val	Ile	Asp	Ala	Ala	Lys	Lys	125

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Ala Lys Glu Ala Gly Ser Thr Arg Phe Cys Met Gly Ala Ala Trp Arg
130 135 140
Asp Thr Ile Gly Arg Lys Thr Asn Phe Ser Gln Ile Leu Glu Tyr Ile
145 150 155 160
Lys Glu Ile Arg Gly Met Gly Met Glu Val Cys Cys Thr Leu Gly Met
165 170 175
Ile Glu Lys Gln Gln Ala Leu Glu Leu Lys Lys Ala Gly Leu Thr Ala
180 185 190
Tyr Asn His Asn Leu Asp Thr Ser Arg Glu Tyr Tyr Pro Asn Val Ile
195 200 205
Thr Thr Arg Ser Tyr Asp Asp Arg Leu Glu Thr Leu Ser His Val Arg
210 215 220
Asp Ala Gly Ile Asn Val Cys Ser Gly Gly Ile Ile Gly Leu Gly Glu
225 230 235 240
Ala Glu Glu Asp Arg Ile Gly Leu Leu His Thr Leu Ala Thr Leu Pro
245 250 255
Ser His Pro Glu Ser Val Pro Ile Asn Ala Leu Leu Ala Val Lys Gly
260 265 270
Thr Pro Leu Glu Asp Gln Lys Pro Val Glu Ile Trp Glu Met Ile Arg
275 280 285
Met Ile Gly Thr Ala Arg Ile Val Met Pro Lys Ala Met Val Arg Leu
290 295 300
Ser Ala Gly Arg Val Arg Phe Ser Met Ser Glu Gln Ala Leu Cys Phe
305 310 315 320
Leu Ala Gly Ala Asn Ser Ile Phe Thr Gly Glu Lys Leu Leu Thr Thr
325 330 335
Pro Asn Asn Asp Phe Asp Ala Asp Gln Leu Met Phe Lys Thr Leu Gly
340 345 350
Leu Ile Pro Lys Pro Pro Ser Phe Ser Glu Asp Asp Ser Glu Ser Glu
355 360 365
Asn Cys Glu Lys Val Ala Ser Ala Ser His
370 375

<210> 34
<211> 362
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 34
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Asp Thr Pro Leu Ile Asp Leu Ile Phe Arg Ala Ala Ser Ile His Arg
35 40 45
Lys Phe His Asp Pro Lys Lys Val Gln Gln Cys Thr Leu Leu Ser Ile
50 55 60
Lys Thr Gly Gly Cys Thr Glu Asp Cys Lys Tyr Cys Ala Gln Ser Ser
65 70 75 80
Arg Tyr Asn Thr Gly Val Lys Ala Thr Lys Leu Met Lys Ile Asp Glu
85 90 95
Val Leu Glu Lys Ala Lys Ile Ala Lys Ala Lys Gly Ser Thr Arg Phe
100 105 110
Cys Met Gly Ser Ala Trp Arg Asp Leu Asn Gly Arg Asn Arg Thr Phe
115 120 125

Lys Asn Ile Leu Glu Ile Ile Lys Glu Val Arg Ser Met Asp Met Glu
 130 135 140
 Val Cys Val Thr Leu Gly Met Leu Asn Glu Gln Ala Lys Glu Leu
 145 150 155 160
 Lys Asp Ala Gly Leu Thr Ala Tyr Asn His Asn Leu Asp Thr Ser Arg
 165 170 175
 Glu Tyr Tyr Ser Lys Ile Ile Ser Thr Arg Thr Tyr Asp Glu Arg Leu
 180 185 190
 Asn Thr Ile Asp Asn Leu Arg Lys Ala Gly Leu Lys Val Cys Ser Gly
 195 200 205
 Gly Ile Leu Gly Leu Gly Glu Lys Lys His Asp Arg Val Gly Leu Ile
 210 215 220
 His Ser Leu Ala Thr Met Pro Thr His Pro Glu Ser Val Pro Phe Asn
 225 230 235 240
 Leu Leu Val Pro Ile Pro Gly Thr Pro Val Gly Asp Ala Val Lys Glu
 245 250 255
 Arg Leu Pro Ile His Pro Phe Leu Arg Ser Ile Ala Thr Ala Arg Ile
 260 265 270
 Cys Met Pro Lys Thr Ile Ile Arg Phe Ala Ala Gly Arg Asn Thr Cys
 275 280 285
 Ser Glu Ser Glu Gln Ala Leu Ala Phe Met Ala Gly Ala Asn Ala Val
 290 295 300
 Phe Thr Gly Glu Lys Met Leu Leu Leu Leu Phe Leu Asp Ser Asp
 305 310 315 320
 Ser Gln Leu Phe Tyr Asn Trp Gly Leu Glu Gly Met Gln Ser Phe Glu
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 Tyr Gly Thr Ser Thr Glu Gly Glu Asp Gly Thr Phe Thr Leu Pro Pro
 340 345 350
 Lys Glu Arg Leu Ala Pro Ser Pro Ser Leu
 355 360

<210> 35
<211> 363
<212> PRT
<213> Schizosaccharomyces pombe

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 Asp Thr Pro Leu Ile Asp Leu Ile Phe Arg Ala Ala Ser Ile His Arg
 35 40 45
 Lys Phe His Asp Pro Lys Lys Val Gln Gln Cys Thr Leu Leu Ser Ile
 50 55 60
 Lys Thr Gly Gly Cys Thr Glu Asp Cys Lys Tyr Cys Ala Gln Ser Ser
 65 70 75 80
 Arg Tyr Asn Thr Gly Val Lys Ala Thr Lys Leu Met Lys Ile Asp Glu
 85 90 95
 Val Leu Glu Lys Ala Lys Ile Ala Lys Ala Lys Gly Ser Thr Arg Phe
 100 105 110
 Cys Met Gly Ser Ala Trp Arg Asp Leu Asn Gly Arg Asn Arg Thr Phe
 115 120 125
 Lys Asn Ile Leu Glu Ile Ile Lys Glu Val Arg Ser Met Asp Met Glu
 130 135 140

Val Cys Val Thr Leu Gly Met Leu Asn Glu Gln Gln Ala Lys Glu Leu
145 150 155 160
Lys Asp Ala Gly Leu Thr Ala Tyr Asn His Asn Leu Asp Thr Ser Arg
165 170 175
Glu Tyr Tyr Ser Lys Ile Ile Ser Thr Arg Thr Tyr Asp Glu Arg Leu
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Asn Thr Ile Asp Asn Leu Arg Lys Ala Gly Leu Lys Val Cys Ser Gly
195 200 205
Gly Ile Leu Gly Leu Gly Glu Lys Lys His Asp Arg Val Gly Leu Ile
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His Ser Leu Ala Thr Met Pro Thr His Pro Glu Ser Val Pro Phe Asn
225 230 235 240
Leu Leu Val Pro Ile Pro Gly Thr Pro Val Gly Asp Ala Val Lys Glu
245 250 255
Arg Leu Pro Ile His Pro Phe Leu Arg Ser Ile Ala Thr Ala Arg Ile
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Cys Met Pro Lys Thr Ile Ile Arg Phe Ala Ala Gly Arg Asn Thr Cys
275 280 285
Ser Glu Ser Glu Gln Ala Leu Ala Phe Met Ala Gly Ala Asn Ala Val
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Phe Thr Gly Glu Lys Met Leu Thr Thr Pro Ala Val Ser Trp Asp Ser
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Asp Ser Gln Leu Phe Tyr Asn Trp Gly Leu Glu Gly Met Gln Ser Phe
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223> Xaa represents any amino acid

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